



Sequence.ST25
SEQUENCE LISTING

<110> Doherty, Joni
Clinton, Gail M.

<120> HER-2 BINDING ANTAGONISTS

<130> 49321-16

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<140> US 09/506,079

<141> 2000-02-16

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<150> US 09/234,208

<151> 1999-01-20

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 79

<212> PRT

<213> Homo sapiens

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<221> MISC_FEATURE

<222> (2)..(2)

<223> Applicants herein disclose Thr and Ser sequence variants at this position

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<222> (5)..(5)

<223> Applicants herein disclose Leu and Pro sequence variants at this position

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<222> (6)..(6)

<223> Applicants herein disclose Pro and Leu sequence variants at this position

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<222> (16)..(16)

<223> Applicants herein disclose Leu and Gln sequence variants at this position

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<222> (18)..(18)

<223> Applicants herein disclose Met and Leu sequence variants at this position

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<221> MISC_FEATURE

<222> (21)..(21)

<223> Applicants herein disclose Gly, Asp, Ala and Val sequence variants at this position

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<221> MISC_FEATURE

Sequence.ST25

<222> (36)..(36)

<223> Applicants herein disclose Leu and Ile sequence variants at this position

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<221> MISC_FEATURE

<222> (54)..(54)

<223> Applicants herein disclose Pro and Arg sequence variants at this position

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<222> (64)..(64)

<223> Applicants herein disclose Pro and Leu sequence variants at this position

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<221> MISC_FEATURE

<222> (73)..(73)

<223> Applicants herein disclose Asp and Asn sequence variants at this position

<400> 1

Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro Xaa
1 5 10 15

Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
20 25 30

Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
35 40 45

Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val Gly Arg Gly Xaa
50 55 60

Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg Tyr Glu Gly

65

70

75

<210> 2

<211> 419

<212> PRT

<213> Homo sapiens

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<221> MISC_FEATURE

<222> (342)..(342)

<223> Applicants herein disclose Thr and Ser sequence variants at this position

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<221> MISC_FEATURE

<222> (345)..(345)

<223> Applicants herein disclose Leu and Pro sequence variants at this position

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<221> MISC_FEATURE

<222> (346)..(346)

<223> Applicants herein disclose Pro and Leu sequence variants at this position

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<222> (356)..(356)

<223> Applicants herein disclose Leu and Gln sequence variants at this position

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<222> (358)..(358)

<223> Applicants herein disclose Met and Leu sequence variants at this position

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<222> (361)..(361)

<223> Applicants herein disclose Gly, Asp, Ala and Val sequence variants at this position

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<222> (376)..(376)

<223> Applicants herein disclose Leu and Ile sequence variants at this position

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<222> (404)..(404)

<223> Applicants herein disclose Pro and Leu sequence variants at this position

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<222> (413)..(413)

<223> Applicants herein disclose Asp and Asn sequence variants at this position

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<222> (394)..(394)

Sequence.ST25

<223> Applicants herein disclose Pro and Arg sequence variants at this position

<400> 2

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
1 5 10 15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Cys Lys
20 25 30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
50 55 60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65 70 75 80

Gln Gly Tyr Val Leu Cys Ala His Asn Gln Val Arg Gln Val Pro Leu
85 90 95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
100 105 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
115 120 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
130 135 140

Leu Thr Glu Cys Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145 150 155 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
165 170 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
180 185 190

His Pro Cys Ser Pro Cys Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
195 200 205

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Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
210 215 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225 230 235 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
245 250 255

His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
260 265 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Cys Pro Asn Pro Glu Gly Arg
275 280 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Lys Leu
290 295 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305 310 315 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
325 330 335

Pro Cys Ala Arg Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val
340 345 350

Pro Val Pro Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser
355 360 365

Phe Leu Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro
370 375 380

Leu Ala Pro Leu Asp Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val
385 390 395 400

Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg
405 410 415

Tyr Glu Gly

<210> 3

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> HER-2-specific oligonucleotide primer

<400> 3
tgagcaccat ggagctggc

19

<210> 4

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> HER-2-specific oligonucleotide primer

<400> 4
tccggcagaa atgccaggct cc

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<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> HER-2 cDNA-specific oligonucleotide primer

<400> 5
aacacagcgg tgtgagaagt gc

22

<210> 6

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<212> DNA

<213> Artificial Sequence

Ins
F8

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<223> HER-2 ECDIIIa-region-specific oligonucleotide primer

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ataccgggac aggtcaacag c

21

<210> 7

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<212> DNA

<213> Artificial Sequence

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<223> HER-2 ECDIIIa-region-specific oligonucleotide primer

<400> 7

tctgggtacc cactcactgc

20

<210> 8

<211> 22

<212> DNA

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<223> HER-2 exon-specific oligonucleotide primer

<400> 8

ttcacactgg cacgtccaga cc

22

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> HER-2 cDNA-specific oligonucleotide primer

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gcacggatcc atagcagact gaggagg

27

<210> 10

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<212> DNA

<213> Homo sapiens

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<221> exon

<222> (1)..(240)

<223> ECDIIIa region coding sequence

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<221> misc_feature

<222> (62)..(62)

<223> Applicants disclose C, T, A and G variants at this position

<400> 10

ggt wcc cac tca cyg cyc ccg agg cca gct gca gtt cct gtc cct cwg 48
Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro Xaa
1 5 10 15

cgc atr cag cct gnc cca gcc cac cct gtc cta tcc ttc ctc aga ccc 96
Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
20 25 30

tct tgg gac mta gtc tct gcc ttc tac tct cta ccc ctg gcc ccc ctc 144
Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
35 40 45

agc cct aca agt gtc cst ata tcc cct gtc agt gtg ggg agg ggc cyg 192
Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val Gly Arg Gly Xaa
50 55 60

gac cct gat gct cat gtg gct gtt sac ctg tcc cgg tat gaa ggc tga 240
Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg Tyr Glu Gly
65 70 75